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ILB 938, a valuable faba bean (*Vicia faba* L.) accession

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Abstract

Here we review the potential of ILB 938 (IG 12132– doi:10.18730/60FD2), a unique faba bean accession originating from the Andean region of Colombia and Ecuador, maintained at ICARDA - International Center for Agricultural Research in the Dry Areas, with resistance to multiple biotic and abiotic stresses and carrying some useful morphological markers. It has been used as a donor of leaf-related drought adaptation traits and chocolate spot (*Botrytis fabae*) resistance genes in faba bean breeding programs worldwide. From generated populations of recombinant inbred lines, QTLs (quantitative traits loci) associated with these useful traits have been mapped. Other markers, such as a lack of stipule-spot pigmentation and clinging pod wall, show the presence of unusual changes in biochemical pathways that may have economic value in the future.

Keywords: germplasm, faba bean, biotic stress, abiotic stress, mapping population

Introduction

Faba bean (*Vicia faba* L.) seeds are a generous source of plant protein, with a global average protein concentration of 29% on a dry-weight basis (Feedipedia, 2018). It is one of the main sources of affordable protein for human consumption in developing countries (consumed as dry or canned), and for livestock feed in many developed countries. The fresh pods and seeds are widely used as a vegetable crop for fresh seed production. Like other legumes, it symbiotically fixes atmospheric nitrogen, thus improving the soil fertility. As a non-host of many cereal pathogens, faba bean is ideal as a break between grain crops in the rotation (Köpke and Nemecek, 2010). It has a mixed breeding system and is cross-pollinated at frequencies of 4-84%, with the value determined by the interaction between the plant genotype, its environment, and the population of pollinators (Bond and Poulsen, 1983). Its interaction with many species of bee (Stoddard and Bond, 1987) makes it suitable for growing in ecological focus areas (Bues *et al*., 2013). It is widely adapted to cool-temperate agriculture, being grown from Mediterranean climates in southern Australia and Mediterranean basin countries to sub-boreal climates in Finland and Canada. Nevertheless, faba bean cultivation is limited due to its susceptibility to several biotic and abiotic constraints globally (*see* Stoddard *et al*., 2006; Torres *et al*., 2006; Khan *et al*., 2010). Hence, genetically diverse sources of resistance genes or genes for specific adaptations such as to abiotic stress factors are required in pre-breeding programs worldwide. Some of these germplasm sources, called 'donors' may become prominent.

Faba bean is represented in germplasm collections by only the cultivated form. Both botanical and molecular data suggest that the wild ancestors of faba bean either have vanished or have not yet been discovered (Maxted, 1993; Duc *et al*., 2010; Kosterin, 2014; Caracuta *et al*., 2016), which highlights the importance of the accessible diversity within the cultivated

form. The place of origin of faba bean is still unknown. A Near or Middle East centre of origin has been proposed (Cubero, 1974), and the earliest identified remains of faba bean date from 10200 BP in a cave in Israel (Caracuta *et al*., 2015). Radiation followed in four directions from the proposed centre: Europe, along the North Africa coast to Spain, along the Nile Valley to Ethiopia, and from Mesopotamia to India and China (Lawes *et al*., 1983). Spanish and European material was taken to South America in the 16th century (Bond, 1976). There are 43,695 faba bean accessions conserved within 37 global genebanks (*ex situ,* FAO, 2010) as well as on-farm conservation (*in situ*, Suso *et al*., 2005). ICARDA (International Center for Agricultural Research in the Dry Areas) hosts the largest collection of over 9,500 accessions (21% of global collection, FAO, 2010). ICARDA maintains its faba bean germplasm in two classes, ILB (International Legume Bean) accessions from different countries, and BPL (Bean Pure Line) accessions that are derived through selfing from accessions drawn from the ILB collection (Saxena and Varma, 1985).

Accession ILB 938

ILB 938 is the result of mass selection from ILB 438 based on seed size. ILB 438 was brought to ICARDA from the Andean region of Ecuador and Columbia (Robertson, 1984). ICARDA's registered BPL derivatives of ILB 438 and ILB 938 are BPL 710 and BPL 1179, respectively. ILB 938/2 is an inbred line developed at Göttingen for use in genetics and breeding studies. The corresponding "IG" number for ILB 938 in the ICARDA genebank is "IG 12132" (accession doi: 10.18730/60FD2, *see* https://www.genesys-pgr.org/10.18730/60FD2). ILB 438 is registered as IG 11632 in the ICARDA genebank (accession doi: 10.18730/601TB).

Morphological markers

68 In the wild-type faba bean, the extra-floral nectary on the stipule is coloured black. The presence
69 of stipule spot pigmentation was proposed as an early morphological marker indicating wild-type
70 'coloured' flowers (tannin-containing faba bean), where there is a black spot on each wing petal
71 and dark vein markings on the standard petal (Picard, 1976). The absence of the pigmentation
72 was considered as the corresponding early morphological indicator for the white-flower, zero-
73 tannin trait (Link *et al*., 2008). ILB 938, however, carries a rare allele (*ssp1*) that decouples
74 pigmentation in flowers from that in stipules, so it has colourless stipules and coloured flowers
75 (Supplementary Figure S1, Khazaei *et al*., 2014a). An Australian line, AF11212, has the same
76 phenotype and is derived from BPL 710 (Dr. Jeff Paull, The University of Adelaide, Australia;
77 personal communication). Crossing ILB 938/2 with AF11212 (including reciprocal crosses)
78 showed in the F1 and F2 generations uniformly the combination of colourless stipule spots and
79 spotted flowers, confirming that the same gene exists in both accessions (Miller, 2016).

80 The seed size of ILB 938 is classified as *equina* (horse bean, field bean, flattened seed;
81 0.6 g / seed) which is expected since it was the medium to large-seeded Mediterranean-adapted
82 faba bean forms that were introduced to Central and South America by immigrants from Spain
83 (Muratova, 1931; Cubero, 1974). The seed coat of ILB 938 is green in colour, which is recessive
84 to the common beige or buff colour (Khazaei *et al*., 2014b).

85 A further noticeable morphological character of ILB 938 is the clinging pod wall, where
86 fibres from the inner epidermis of the pod cling to the surface of the seed (Supplementary Figure
87 S2). We have not seen this trait otherwise reported in faba bean germplasm, and while it is of
88 little importance agronomically or economically, it may indicate a difference in cell wall
89 development that has other impacts elsewhere in the plant or in the value chain.

90 Finally, the funiculus is yellow in ILB 938, in contrast to the common green displayed by
91 other accessions.

92 **Biotic stresses**

93 The resistance of ILB 938 to chocolate spot (CS, caused by *Botrytis fabae* Speg.) has been
94 demonstrated in Egypt (Mohamed *et al*., 1981 [re-coded NEB 938]; Khalil and Nassib, 1984;
95 Robertson, 1984), Syria (Hanounik, 1982), the United Kingdom (Jellis *et al*., 1982), Canada
96 (Robertson, 1984), France (Tivoli *et al*., 1988), and Ethiopia (Beyene *et al*., 2016). Further, we
97 have noticed its resistance to CS in field conditions of both southern Finland and western
98 Canada.

99 The resistance of the original source of ILB 938 was confirmed in the Nile Delta after
100 crosses with the local cultivar Giza 3 (ICARDA Caravan, 1998; Zeid *et al*., 2009). From there it
101 was transferred to locally adapted material that was released as Giza 461 in Egypt (Bond *et al*.,
102 1994; Dwivedi *et al*., 2006; El-Komy *et al*., 2015).

103 The related bean pure lines BPL 710 and BPL 1179 to ILB 438 and ILB 938, respectively
104 also showed high resistance to CS across environments (Hanounik and Maliha, 1986; Hanounik
105 and Robertson, 1988; Villegas-Fernández *et al*., 2012). The Australian cultivar Icarus was
106 derived from BPL 710 and released as a cultivar resistant to CS and rust (Dwivedi *et al*., 2006).

107 ILB 938 is, furthermore, considered as a consistent source of resistance to rust (*Uromyces*
108 *viciae-fabae* (Pers.) J. Schrot.) (Rashid and Bernier, 1991; Khalil *et al*., 1985; Rashid and
109 Bernier, 1986). Both BPL 710 (Australian accession No. AC1269) and BPL 1179 (AC1272) are

110 registered as rust-resistant accessions in Australia (Ijaz *et al*., 2018) as well as in ICARDA
111 (1987).

112 Some studies have suggested that ILB 938 may also carry resistance to crenate
113 broomrape, *Orobanche crenata* Forsk., an achlorophyllous, holoparasitic weed, poses a major
114 constraint to faba bean production in Mediterranean climates (Zeid *et al*., 2006; 2009).

115 **Abiotic stresses**

116 Drought adaptation is an essential character for faba bean cultivation in arid and semiarid
117 regions. ILB 938 has demonstrated high water use efficiency (WUE) in several studies (e.g.,
118 Abdelmula *et al*., 1999; Link *et al*., 1999; Stoddard *et al*., 2006; Khan *et al*., 2007, 2010; Khazaei
119 *et al*., 2013; Khazaei *et al*., 2014b) mainly due to low stomatal conductance, thus minimizing
120 water loss and maintaining yield under drought conditions. Nevertheless, its reduced leaf
121 stomatal conductance was not associated with a highly ramified rooting system (Belachew *et al*.,
122 2018).

123 While ILB 938 has relatively low productivity, no yield penalty was observed when it
124 was exposed to drought conditions (Link *et al*., 1999; Khan *et al*., 2007; Khazaei *et al*., 2014b).
125 It maintains a relatively high water status under water deficit conditions, demonstrating high
126 WUE with relatively low yield, because its stomata shut early, reducing potential photosynthesis
127 while limiting water loss.

128 The response of ILB 938/2 to ultraviolet light differs greatly from that of a contrasting
129 cultivar, Aurora/2 that was developed at low altitudes and high latitudes where incident UV is
130 much weaker than high in the Andes (Yan *et al*., 2018).

Mapping populations

A population of recombinant inbred lines (RILs) was developed from the cross of Mélodie/2 × ILB 938/2 (along with its reciprocal) at the University of Helsinki (Khazaei *et al*., 2014a). This population has been mapped for traits related to drought adaptation (Khazaei *et al*., 2014b), vicine-convicine concentration (v-c, Khazaei *et al*., 2015), and stipule spot pigmentation (Khazaei *et al*., 2014a). QTLs (quantitative traits loci) for seed size, seed coat colour, clinging pod wall and yellow funiculus have also been located. ILB 938 and Mélodie differed at two loci affecting stomatal activity at opposite ends of Chromosome II, with each parent contributing a canopy-cooling allele (Khazaei *et al*., 2014b). The progenies of this population facilitated the development of a reliable molecular marker for v-c in this crop (Khazaei *et al*., 2017). This population is being phenotyped for salinity response in a collaboration with Egypt and collaborative studies on other traits are in progress. Near-isogenic lines have been derived from heterozygous F5 individuals at Göttingen (Tacke and Link, 2017).

Another RIL population, ILB 938/2 × Disco/2 (Khazaei *et al*., 2014a), is suitable for CS genetic studies. Disco (low in both tannin and v-c) has been shown to be very sensitive to CS (Villegas-Fernández *et al*., 2012; Khazaei, Personal observation). A RIL population from ILB 938/2 × Aurora/2 (Khazaei *et al*., 2014a) will be useful for analyzing the basis of the difference in ultraviolet response of these two lines.

A multi-parent population [(Disco/2 × ILB 938/2) × (IG 114476 × IG 132238)] has been prepared for use in genomic studies (Khazaei *et al*., 2018). This population is at F4 generation at the time of writing this paper and kept at the University of Reading, UK.

DNA fingerprinting

ILB 938/2 was genotyped using 875 SNP (single nucleotide polymorphism) markers developed by Webb *et al*. (2016). The results showed a high level of homozygosity (99.6%, Webb *et al*., 2016). The genotyping calls on ILB 938/2 are presented in Supplementary Table S1.

Conclusions

The presence of unusual traits in this material is intriguing, because the crop has been grown in South America for only about 500 of its 10 000 years of domestication. It may be attributable to several causes, including widespread genetic variation introduced by the European settlers, adaptation to extremely varied environments within short distances due to altitude, frequent gene exchanges by pollinators and movement of peoples, and natural selection (Bond *et al*., 1994), or UV-induced mutation. Recently, several new accessions from Spain, Ecuador, Colombia and Peru with high level of resistance to CS were identified (Maalouf *et al*., 2016).

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